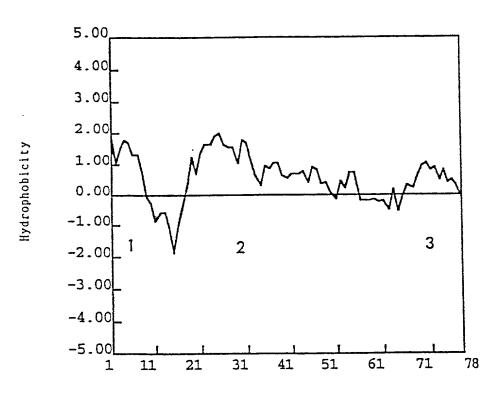
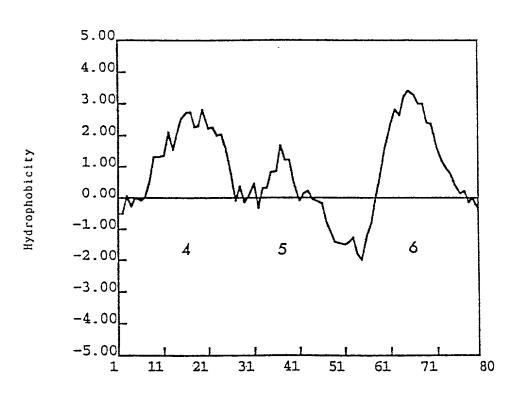
5'	GIG	ccc	10 ATG	crg	œc					TGT				TTC	46 AAG	AAC	CAG	55 CGA
									Val	Cys	His	Val	Ile	Phe	ГУЗ	Asn	Gln	Arg
			64			73			82			91			100			109
	ATG	CAC	TCG	ccc	ACC	ACC	arc	TTC	ATC	GIC	AAC	CTG	GCA	GIT	ecc	GAC	ATA	ATG
	Met	His	Ser	Ala	Thr	Ser	Leu	Phe	Ile	Val	Asn	Leu	Ala	Val	Ala	Asp	Ile	Met
			118												154			163
	ATC	ACG	CIG	CTC	AAC	ACC	<u></u>	TIC	ACT	TTG	GIT	œc	TTT	GIG	AAC	AGC	ACA	TGG
١	Ile	Thr	Leu	Leu	Asn	Thr	Pro	Phe	Thr	Leu	Val	Arg	Phe	Val	Asn	Ser	Thr	Trp
			172			181			190			199			208			217
	ATA	TIT	CCC	AAG	œc	ATG	TGC	CAT	GIC	AGC	CCC	TTT	GCC	CAG	TAC	TGC	TCA	CIG
	Ile	Phe	Gly	Lys	Gly	Met	Cys	His	Val	Ser	Arg	Phe	Ala	Gln	Tyr	CAa	Ser	Leu
	CAC	CIV.	226	CCA	CIG	235	٠, ٢											
							_											
	His	Val	Ser	Ala	Leu	Thr												

5'	GAG	CCA	9 GCT									36 TTG				ATC	CIG	54 CTC
	Glu	Pro	Ala	Asp	Leu	Phe	qxT q	Lys	Asn	Leu	Asp	Leu	Pro	Thr	Phe	Ile	Leu	Leu
	AAC	ATC	63 CTG	ccc	crc							90 TAC					aag	108 AAA
	Asn	Ile	Leu	Pro	Leu	Leu	Ile	Ile	Ser	Val	Ala	Tyr	Val	Arg	Val	Thr	Lys	Lys
	CIG	TGG	117 CIG	TGT								144 ACA				TIT	GCC	162 CTG
	Leu	Trp	Leu	CÀa	Asn	Met	Ile	Val	Asp	Val	Thr	Thr	Glu	Gln	Tyr	Phe	Ala	Leu
١	CGG	ccc	171 AAA	AAG							TTG		CIG	GIG	207 GTA	GIC	CTC	216 TTT
	Arg	Pro	Lys	Lys	Lys	Lys	Thr	Ile	Lys	Met	Leu	Met	Leu	Val	Val	Val	Leu	Phe —
		CTC Leu		TGG					3,									

Fig. 3



The position in the amino acid sequence

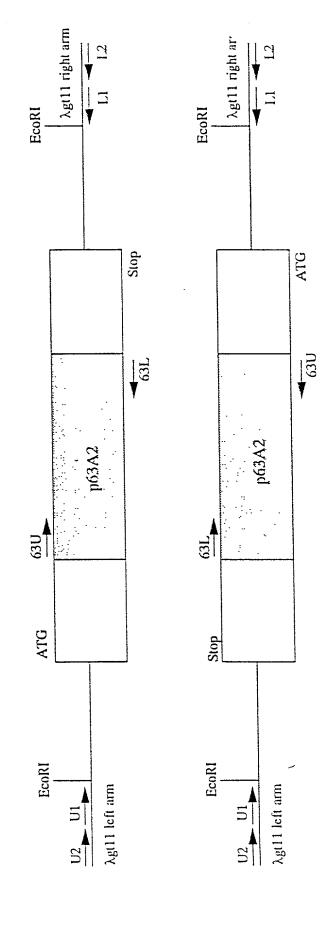


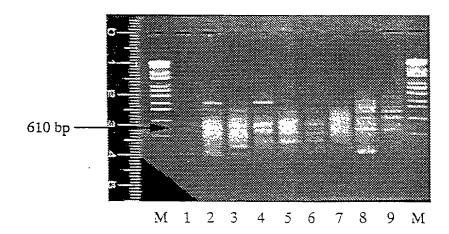
The position in the amino acid sequence

Fig. 5

10	20	30	40	50	
. VCHVIFKNOR	MHSATSLFIV	NLAVADIMIT	LLNTPFTLVR	หวังสำนังกรทั้งเรี	50
. VCHVIFKNOR	MHSATSLFIV	NLAVADIMIT	LLNTPFTLVR	FVNST/VFGK	50
- Service Company of the St.	70	80	90	100	
					100
GMCHVSRF4Q	YCSLHVSALT	LTAIAVDRHQ	VIMHPLKPRI	SITKGVIYLA	100
110			,		
110	120	130		150	
TITLE BAS MODO	7 700 700 70				150
VIWVMATEES	LPHAICQKLF	TFKYSEDIVR	SLCLPDFPER	WDremkarbri	150
160	170	100	100	200	
	II TTENNAME	TAU			222
ATETILIVITE	Αντιαίτατας Θ	AT VET MICHAE			200
***************************************	# ##SXUTUE	XV VVVTI ATTOM	Transtition	WITCH STATE	200
210	220	230	240	250	
KMIMEVVVI!			240	250	250
KMLVLVVVII.					250
	VCHVIFNOR VCHVIFNOR 60 GMCHVSRFAC GMCHVSRFAC 110 VIWVMATFFS 160 PTFILINIER ATFILLYLER 210 RVIMLYVVL	VCHVIFKNOR MHSATSLFIV VCHVIFKNOR MHSATSLFIV 60 70 GMCHVSRFAC VCSLHVSALT 110 120 VIWVMATFFS LPHAICQKLF 160 170 PIFFILINILP LLITSVAVAR ATFILLYLLP LFILSVAVAR 210 220 KMMLVVVL	VCHVIFKNOR MHSATSLETV NIAVADIMITE VCHVIFKNOR MHSATSLETV NIAVADIMITE 60 70 80 GMCHVSRFAC VCSLHVSALT LTALAVDRHQ 110 120 130 VIWVMATFFS LPHAICQKLF TFKYSEDIVR 160 170 180 PTFILINIE LLITSVAVAR VAKKLVICAM ATFILLYLLE LFITSVAVAR VAKKLVICAM ATFILLYLLE LFITSVAVAR VAKKLVICAM 210 220 230 KVIMLVVVI.	VCHVIFFNOR MHSATSLFIV NLAVADIMITI LLNTPFTLVR VCHVIFFNOR MHSATSLFIV NLAVADIMITI LLNTPFTLVR 60 70 80 90 GMCHVSRFAC VCSLHVSALT LTALAVDRHQ VIMHPLKPRI 110 120 130 140 EF VIWVMATFFS LPHAICQKLF TFKYSEDIVR SLCLPDFPEP 160 170 180 190 PTFILLNIËF LLIISVAVAR VAKKLWICHM TVDVITEQYF ATFILLYLLE LFIISVAVAR VAKKLWICHT IGDVITEQYL 210 220 230 240 KMIMLVVVI!	VCHVIFKNOR MHSATSLFIV NLAVADIMITI LLNTPFTLVR EVNSTWIFGK VCHVIFKNOR MHSATSLFIV NLAVADIMITI LLNTPFTLVR EVNSTWIFGK 60 70 80 90 100 GMCHVSRFAQ VCSLHVSALII LTALAVDRHQ VIMHPLKPRI SITKGVIYLA 110 120 130 140 150 EP ADLEWKNLDLI VIWVMATFFS LPHAICOKLF TFKYSEDIVR SLCLPDFPEP ADLEWKYLDLI 160 170 180 190 200 PTFILLNILP LHIISVAVAR VAKKLVICAN IGDVITEQYF ALRPKKKTI ATFILLYLLP LFIISVAVAR VAKKLVICAN IGDVITEQYL ALRRKKKTIV 210 220 230 240 250 KMIMLVVIL







 $M: \lambda DNA/Sty I$ marker

lane 1; 63U~63L

lane 2; U1~63U

lane 3; U1~63L

lane 4: U2~63U

lane 5; U2~63L

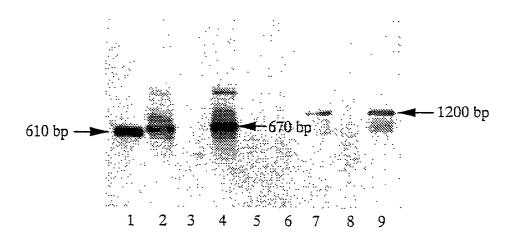
lane 6; L1~63U

lane 7; L1~63L

lane 8; L2~63U

lane 9; L2~63L

Fig. 8



lane 1; 63U~63L

lane 2; U1~63U

lane 3; U1~63L

lane 4; U2~63U

lane 5; U2~63L lane 6; L1~63U

lane 7; L1~63L

lane 8; L2~63U

lane 9; L2~63L

```
1.0
                          20
                                 30
                                         40
           GGGCCCCCTTACACCCTTTGTGATTGAGATCCGGGGTTTC-AAGGGGTGCATGATGAAG
63A2-5'. SEQ
           GGGCTTCCTCTGTGCCCCGTGCCCCTCGCTCCCAGGCTCCCTCTGTGGTGTGGACTCCTC
MUSGIR. DNA
          130
                  140
                          150
                                  160
                                         170
                                                  180
          60
                  70
                          80
                                  90
                                          100
                                                  110
63A2-5'. SEQ
           GACTAAGCCACAATGAGCAGGGCTTTCACCGTGGGGTTCTGGGACTCAGCGCCCTAGCGC
               MUSGIR. DNA
           TAGCCCGGTGCGCTCAGC--CCCTCGCACC-CAGCCTCCAGGCACAGAGCCCGGCAGGGA
          190
                  200
                            210
                                    220
                                           230
         120
                                150
                 130
                          140
                                         160
63A2-5'. SEQ
           TTCCTGCCCACAAAGTTCTCC<u>CAGGGGAGGGGTGGCTCCTGCAAAATG</u>GTCCCTCACCTC
             : :::: : :: :: :::::::
                                           MUSGIR, DNA
           GCTCAGCCC----TTGTGCCTAGAGCTGCAGTGGCT-GGACATGAAGGTTCCTCCTGTC
                         260
                                 270
                                         280
                                                 238 mouse GIR
         180
                 190
                         200
                                  210
                                         220
                                                  230 initiation codon
63A2-5'. SEQ
           TTGCTGCTCTCCCCCTTGGTGCGAGCCACGAGCCCCACGAGGGCCGGGCCGAC
           CTGCTTCTCTTCTGTCCTCAGTGCGAGCTACTGAGCAACCGCAGGTCGTCACTGAG
MUSGIR. DNA
         300
                 310
                         320
                                 330
                                         340
                                                  350
         240
                 250
                          260
                                 270
                                         280
                                                  290
63A2-5'. SEQ
           GAGCAGAGCGCGGAGGCGGCCCTGGCCGTGCCCAATGCCTCGCACTTCTTCTCTTGGAAC
           MUSGIR. DNA
           CATCCCAGCATGGAGGCAGCCCTGACCGGGCCCAACGCCTCCTCGCACTTC---TGGGCC
         360
                 370
                         380
                                 390
                                         400
                                                 410
         300
                 310
                          320
                                  330
                                         340
                                                  350
63A2-5' . SEQ
           AACTACACCTTCTCCGACTGGCAGAACTTTGTGGGCAGGAGGTGCTACGGCGCTGAGTCC
           MUSGIR. DNA
           AACTACACTTTCTCTGACTGGCAGAACTTCGTGGGCAGGAGACGTTATGGGGCCGAGTCC
            420
                   430
                           440
                                    450
                                           460
                                                   470
         360
                         380
63A2-5'. SEQ
           CAGAACCCCACGGTGAAAGCCCTGCTC
           CAGAACCCCACGGTGAAAGCACTGCTC
MUSGIR. DNA
           480
                   490
```

		10	20	30	40	50 60
OR16-F. SEQ	TTGCCCC	TCCYCATC.	ATCTCTGTGG	CCTACGCYCGI	TGTGGCCAARA	AACTGTGGCTGTGT
	: :: :	:: .:::	:::::	:::: ::::::	:::::::::::::::::::::::::::::::::::::::	: ::::::: :::
MUSGIR. DNA	CTTCCAC	TCTTCATT.	ATCTCAGTGG	CCTATGCTCGT	TGTGGCCAAGA	AGCTGTGGCTCTGT
	1030	1040	1050	1060	1070	1080
		70	80	90	100	110
OR16-F. SEQ	AATATGA	TTGGCGAT	GTGACCACAG	AGCAGTACTT	rg-cctkcggc	GCAAAAAGAAGAAG
•	- :: :	::::::	:::::::::::	::::::::	; X::.:::	:::: ::::::
MUSGIR. DNA	YYCYCCY	TTGGCGAC	GTGACCACAG	AGCAGTACCT(CGCCCTGCGAC	GCAAGAAGAAGACC
	1090			1120		1140
	120	130	140	150	160	170
OR16-F. SEQ	ACCATCA	AGATGTTG.	ATGCTGGTGG	TAGTCCCCTT	TGCCCTCCGCT	GGTTCCCCCTCAAC
	::: : :	:::::	:::: ::::	:::::	:::::::	:::::::
MUSGIR. DNA	ACCGTGA	AGATGCTG	GTGCTTGTGG	TAGTCCTCTT	TGCCCTCTGCT	GGTTCCCTCTCAAC
	1150	1160	1170	1180	1190	1200
•	180	190	200	210		
OR16-F.\SEQ	TGCTACG	TCCTCCTC	CTGTCCAGCA	AGGTCATCCG	C	
	::::::	::::::	::::::::	::: :::X	:	
MUSGIR. DNA	TGCTATG	TCCTCCTC	TTGTCCAGCA	AGGCCATCCA	C	
	1210	1220	1230	1240		

Fig. 11

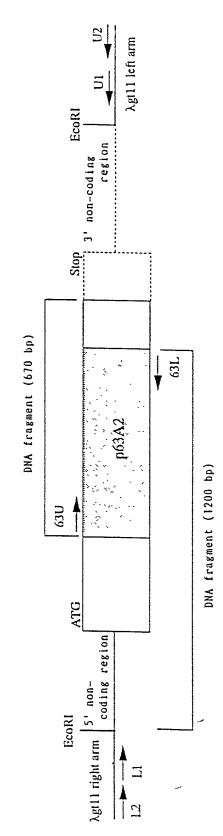
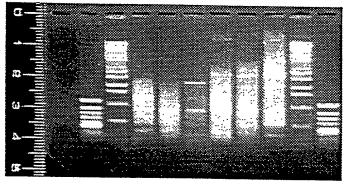


Fig. 12



M1 M2 1 2 3 4 5 6 M2 M1

M1; $\phi X174/HincII$

M2; $\lambda/StyI$

lane 1; 63U~Anchor Primer

lane 2; 63-6~Anchor Primer

lane 3; 63-7~Anchor Primer

lane 4; 63-6~Anchor Primer

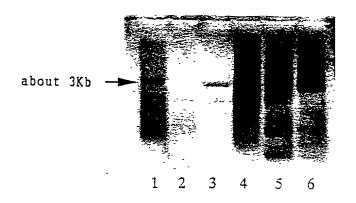
lane 5; 63-7~Anchor Primer

lane 6; 63-8~Anchor Primer

Primary PCR

Secondary PCR

Fig. 13



lane 1; 63U~Anchor Primer

lane 2; 63-6~Anchor Primer

lane 3; 63-7~Anchor Primer

lane 4; 63-6~Anchor Primer

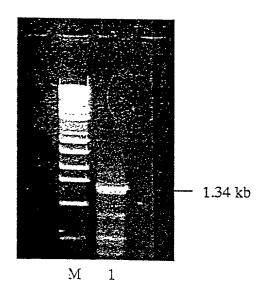
lane 5; 63-7~Anchor Primer

lane 6; 63-8~Anchor Primer

Primary PCR

Secondary PCR

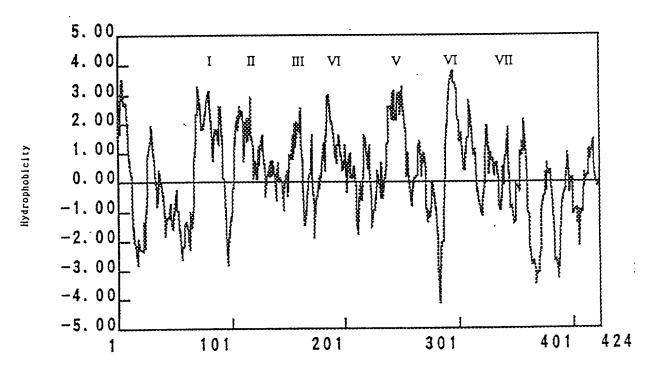
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63A2-3'. seq				. •	CAAGGTCATCCGCA
00AL 0 . 30Q			:::::::		
MUSGIR. DNA					CAAGGCCATCCACA
	1190		1210 122		1240
	70	80	90	100	110 120
63A2-3'. seq	CCAACAATGCC	CTCTACTTTG	CCTTCCACTGGTT	TGCCATGAGCAG	CACCTGCTATAACC
•	:::::::::::::::::::::::::::::::::::::::		:::::::::::::::::::::::::::::::::::::::	:::::::::::::::::::::::::::::::::::::::	:: :: ::::::
MUSGIR. DNA	CCAACAATGCC	CTCTACTTTG	CCTTCCACTGGTT	FGCCATGAGCAG	TACTTGTTATAACC
	1250	1260	1270 128	0 1290	1300
	130	140	150	160	170 180
63Å2-3'. seq	CCTTCATATAC	TGCTGGCTGA	ACGAGAACTTCAG	SATTGAGCTAAA	GGCATTACTGAGCA
	:::::::	:::::::::::::::::::::::::::::::::::::::	: ::::::::	: :::::::	::::::
MUSGIR. DNA	CCTTCATCTAC	TGCTGGCTCA	ATGAGAACTTTAG	GTTGAGCTTAA	GGCATTGCTGAGCA
	1310	1320	1330 134	0 1350	1360
	. 190	200	210	220	230 240
63A2-3'. saq	TGTGTCAAAGA	CCTCCCAAGC	CTCAGGAGGACAG	CONCOCTOCCO	AGTTCCTTCCTTCA
1	:::: :::::		: ::::: :::::		
MUSGIR. DNA	TGTGCCAAAGG				AGTTCCTTCCTTCA
	1370	1380	1390 140	•	1420
	250	260	270	280	290 300
63A2-3'. seq	GGGTGGCCTGG	IACAGAGAAGAA			CAATAACCTCCTGC
		:::::::::			::: ::: : :::
MUSGIR. DNA	GGGTGGCATGG	iacagagaaga	BCCATGGTCGGAG	GCTCCACTACC	TAATCACCACTTGC
	1430	1440	1450 146	3 1470	1480
	310	320	330	340	350 360
6212 2'					ACCCATTGTGACGA
63 A 2-3'. seq					
MUSGIR. DNA	:: : ::::: ccrcrrcccic				
MUSGIR. DRA		***********		::::::::::::::::::::::::::::::::::::::	
			GGAAGACAGATCT	STCATCTGTGGA.	ACCCGTTGTGGCCA
	1490	1500	GGAAGACAGATCT	STCATCTGTGGA.	ACCCGTTGTGGCCA 1540
. 6212-21 000	1490 _370	1500	390 390	STCATCTGTGGA. 1530 400	ACCCGTTGTGGCCA 1540 410
63A2-3'.seq	1490 370 TGAGTTAGAAG	1500 380 AG <u>gttgggaa</u>	GGAAGACAGATCT(1510- 1:52 390 GAGGGAGTGGGAG	STCATCTGTGGA D 1530 400 GGGTCTGT-CTC	ACCCGTTGTGGCCA 1540
•	1490 370 TGAGT(AGAAG	1500 380 GAG <u>GTTGGGAA</u> G	GGAAGACAGATCT 1510 1:52 390 GAGGGAGTGGGAG	STCATCTGTGGA 1530 400 GGGTCTGT-CTC	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG
MUSGIR. DNA	1490 370 TGAGTTAGAAG ::::::: TGAGTTAGGGA	1500 380 GAG <u>GTTGGGAAC</u> : : ::::: AAGCT-GGAAC	GGAAGACAGATCT(1510 152 390 GAGGGAGTGGGAG(: :: :::::: GTTGGTGGGGGAG	TCATCTGTGGA 1530 400 GGGTCTGT-CTC :::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: :::: TCACAATTGACCAG
•	1490 370 TGAGT(AGAAG ::::::: TGAGT(AGGGA 1550 A	380 380 38 <u>GTTGGGAA</u> : : : :::: AAGCT-GGAAC 1560	GGAAGACAGATCT(1510 152 390 GAGGGAGTGGGAG(: :: ::::: GTTGGTGGGGGGAG(1570 15	TCATCTGTGGA 1530 400 GGGTCTGT-CTC IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: ::: TCACAATTGACCAG 1600
MUSGIR, DNA	1490 TGAGT(AGAAG :::::::: TGAGT(AGGAA 1550 A	1500 380 GAG <u>GTTGGGAAC</u> : : ::::: AAGCT-GGAAC 1560 430	GGAAGACAGATCT(1510 152 390 GAGGGAGTGGGAG : :: ::::: GTTGGTGGGGGGAG(1570 15	TCATCTGTGGA. 1530 400 GGGTCTGT-CTC ::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: : ::: TCACAATTGACCAG 1600 0 470
MUSGIR. DNA	1490 370 TGAGTTAGAAG :::::::: TGAGTTAGGGA 1550 A 420 GGAAAGAGA	1500 380 GAG <u>GTTGGGAAC</u> : : : ::::: AAGCT-GGAAC 1560 430 AG-CCTATTCTC	GGAAGACAGATCTO 1510 152 390 GAGGGAGTGGGAG 1111 1111 1111 1111 1111	TCATCTGTGGA 1530 400 GGGTCTGT-CTC :::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: ::: TCACAATTGACCAG 1600
MUSGIR. DNA mouse GIR stop codon 63A2-3'. seq	1490 TGAGT(AGAAG :::::::: TGAGT(AGGAA 1550 A 420 GGAAAGAGA ::::::	1500 380 GAGGTTGGGAAC : : ::::: AAGCT-GGAAC 1560 430 AG-CCTATTCTC	GGAAGACAGATCT(1510 152	TCATCTGTGGA. 1530 400 GGGTCTGT-CTC ::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: : ::: TCACAATTGACCAG 1600 0 470 AAACACACTCCTGC
MUSGIR, DNA	1490 TGAGT(AGAAG :::::::: TGAGT(AGGGA 1550 A 420 GGAAAGAGA :::::: ACACTAACAGA	380 380 380 380 380 380 380 380 380 380	GGAAGACAGATCT(1510 152	TCATCTGTGGA. 1530 400 GGGTCTGT-CTC ::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: : ::: TCACAATTGACCAG 1600 0 470 AAACACACTCCTGC GGTTCCTAGGAACC
MUSGIR. DNA mouse GIR stop codon 63A2-3'. seq	1490 TGAGT(AGAAG :::::::: TGAGT(AGGAA 1550 A 420 GGAAAGAGA :::::: ACACTAACAGA	380 380 380 380 380 380 380 380 380 380	GGAAGACAGATCT(1510 152	TCATCTGTGGA. 1530 400 GGGTCTGT-CTC ::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: : ::: TCACAATTGACCAG 1600 0 470 AAACACACTCCTGC GGTTCCTAGGAACC
MUSGIR. DNA mouse GIR stop codon 63A2-3'. seq MUSGIR. DNA	1490 TGAGT(AGAAG ::::::::: TGAGT(AGGAA 1550 A 420 GGAAAGAGA :::::: ACACTAACAGA 1610 480	380 380 380 380 380 380 380 380 380 380	GGAAGACAGATCT6 1510 152 390 GAGGGAGTGGGAG6 : :: ::::: GTTGGTGGGGGAG6 1570 15 440 CACACATGATC-T ::::: : AACACAGAAGCAG 1630 16	TCATCTGTGGA. 1530 400 GGGTCTGT-CTC ::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: : ::: TCACAATTGACCAG 1600 0 470 AAACACACTCCTGC GGTTCCTAGGAACC
MUSGIR. DNA mouse GIR stop codon 63A2-3'. seq	1490 TGAGT(AGAAG :::::::: TGAGT(AGGAA 1550 A 420 GGAAAGAGA :::::: ACACTAACAGA	380 380 380 380 380 380 380 380 380 380	GGAAGACAGATCT6 1510 152 390 GAGGGAGTGGGAG6 : :: ::::: GTTGGTGGGGGAG6 1570 15 440 CACACATGATC-T ::::: : AACACAGAAGCAG 1630 16	TCATCTGTGGA. 1530 400 GGGTCTGT-CTC ::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: : ::: TCACAATTGACCAG 1600 0 470 AAACACACTCCTGC GGTTCCTAGGAACC
MUSGIR. DNA mouse GIR stop codon 63A2-3'. seq MUSGIR. DNA 63A2-3'. seq	1490 TGAGT(AGAAG ::::::::: TGAGT(AGGAA 1550 A 420 GGAAAGAGA :::::: ACACTAACAGA 1610 480 AGAAGCTGTAG	380 380 380 380 380 380 380 380 380 380	GGAAGACAGATCT6 1510 152 390 GAGGGAGTGGGAG6 1570 15 440 CACACATGATC-T ::::::::: AACACAGAAGCAG	TCATCTGTGGA. 1530 400 GGGTCTGT-CTC ::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: : ::: TCACAATTGACCAG 1600 0 470 AAACACACTCCTGC GGTTCCTAGGAACC
MUSGIR. DNA mouse GIR stop codon 63A2-3'. seq MUSGIR. DNA	1490 TGAGT(AGAAG ::::::::: TGAGT(AGGAA 1550 A 420 GGAAAGAGA :::::: ACACTAACAGA 1610 480	380 380 380 380 380 380 380 380 380 380	GGAAGACAGATCT6 1510 152 390 GAGGGAGTGGGAG6 1570 15 440 CACACATGATC-T ::::::::: AACACAGAAGCAG	TCATCTGTGGA. 1530 400 GGGTCTGT-CTC ::::::::::::::::::::::::::::::::::	ACCCGTTGTGGCCA 1540 410 -CAC-CTGAGGCAG ::: : ::: TCACAATTGACCAG 1600 0 470 AAACACACTCCTGC GGTTCCTAGGAACC



 $\begin{array}{l} M \ ; \ \lambda \, / \, StyI \\ lane \ 1 \ ; \ Whole \ Brain \end{array}$

5'.	ATG	GTC	g CCT	CAC	СТС	18 TTG	CTG	стс	27 TGT	стс	CTC	3 6 CCC	TTG	GTG	45 CGA	GCC	ACC	54 GAG
													 Leu					
	CCC	CAC	63 GAG	GGC	cgg	72 GCC	GAC	GAG	81 CAG	AGC	GCG	9 0 G A G	GCG	GCC	9 9 CTG	GCC	GTG	108 CCC
	Pro	His	Glu	Gly	Arg	Ala	Asp	Glu	Gln	Ser	Ala	Glu	Ala	Ala	Leu	Ala	 V a I	Pro
	AAT	GCC	117 TCG	CAC	TTC	126 TTC	TCT	TGG	135 AAC	AAC	TAC	144 ACC	TTC	TCC	153 GAC	TGG	CAG	162 AAC
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	CTG	CTC	225 ATT	GTG	GCT	234 TAC	TCC		243 ATC		GTC	252 TTC	TCA	CTC	261 TTT	GGC	AAC	270 GTC
	Leu	Leu	11e	Ya i	Ala	Туг	Ser	Phe	I le	110	Val		Ser	Leu	Phe	Gly	Asn	Vai
	CTG	GTC	279 TGT	CAT	GTC	288 ATC	TTC	AAG	297 AAC	CAG	CGA	306 ATG	CAC	TCG	315 GCC	ACC	AGC	324 CTC
	Lau	V a I	Cys	His	V a i	i i a	Phe	Lys	Asn	Gin	Årg	Met	His	Ser	Ala	Thr	Ser	Leu
	TTC	ATC	333 GTC	AAC	CTG	342 GCA	GTT	GCC	351 GAC	ATA	ATG	360 ATC	ACG	CTG	369 CTC	AAC	YCC	378 CCC
	Phe	Ha	Vai	Åsn	Leu	Ala	V a [Ala	Asp	lia	Met	lla	Thr	Leu	Leu	Asn	Thr	Pro
	TTC	ACT	387 TTG	GTT	CGC	396 TTT	GTG	AAC	405 AGC	ACA	TGG	414 ATA	TTT	GGG	423 AAG	GGC	ATG	432 TGC
	Phe	Thr	Leu	V a i	Arg	Phe	l s V	Åsn	Ser	Thr	Trp	110	Phe	Gly	Lys	Gly	Met	Cys
	CAT	GTC	441 AGC	CGC	TTT		CAG			TCA	CTG	468 CAC	GTC	TCA	477 GCA	CTG	ACA	486 CTG
	His	Yai	Ser	Arg	Phe	Ala	Gin	Туг	Суз	Ser	Leu	Нis	Val	Ser	Ala	Leu	Thr	Lau
	ACA	GCC	495 ATT	GCG	GTG	504 GAT	CGC	CAC	513 CAG	GTC	ATC	522 ATG	CAC	ccc	531 TTG	AAA	ccc	540 CGG
	Thr	Ala	He	Ala	V a i	Asp	Årg	His	Gln	Val	He	Met	His	Pro	Leu	Lys	Pro	Årg
	ATC	TCA	549 ATC	ACA	AAG	558 GGT	GTC	ATC	567 TAC	ATC	GCT	576 GTC	ATC	TGG	585 ACC	ATG	GCT	594 ACG
	110	Ser	110	Thr	Lys	Gly	I s Y	lle	Tyr	i i e	Ala	V a l	110	Trp	Thr	Met	Ala	Thr
	TTC	TTT	603 TCA	CTC	CCA	612 CAT	GCT	ATC	621 TGC	CAG	***	0E6	TTT	ACC	639 TTC	***	TAC	648 AGT
	Phe	Phe	Ser	Leu	Pro	His	Ala	I i e	Cy 5	Gin	Lys	Leu	Pho	Thr	Phe	Lys	Tyr	Ser
	GAG	GAC	657 ATT	GTG	CGC	666 TCC	CTC	TGC	675 CTG	CCA	GAC	684 TTC	CCT	GAG	693 CCA	GCT	GAC	702 CTC
	Glu	Asp	110	Yal	Arg	Ser	Leu	Cys	Leu	Pro	Asp	Phe	Pro	Glu	Pro	Ala	Asp	Leu

720 729 738 TTC TGG AAG TAC CTG GAC TTG GCC ACC TTC ATC CTG CTC TAC ATC CTG CCC CTC Phe Trp Lys Tyr Leu Asp Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu 774 783 792 801 CTC ATC ATC TCT GTG GCC TAC GCT CGT GTG GCC AAG AAA CTG TGG CTG TGT AAT --- --- --- --- --- --- --- --- --- --- --- --- --- ---Leu ile ile Ser Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn 819 828 837 846 855 ATG ATT GGC GAT GTG ACC ACA GAG CAG TAC TIT GCC CTG CGG CGC AAA AAG AAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---Met lie Gly Asp Vai Thr Thr Glu Gin Tyr Phe Ala Leu Arg Arg Lys Lys Lys 882 891 900 909 AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT GCC CTC TGC TGG TTC Lys Thr lie Lys Met Leu Met Leu Vai Vai Val Leu Phe Ala Leu Cys Trp Phe 936 945 954 963 CCC CTC AAC TGC TAC GTC CTC CTC CTG TCC AGC AAG GTC ATC CGC ACC AAC AAT Pro Leu Asn Cys Tyr Val Leu Leu Ser Ser Lys Val 11e Arg Thr Asn Asn 990 999 1008 1017 GCC CTC TAC TIT GCC TIC CAC TGG TIT GCC ATG AGC AGC ACC TGC TAT AAC CCC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser Ser Thr Cys Tyr Asn Pro 1044 1053 1062 1071 TTC ATA TAC TGC TGG CTG AAC GAG AAC TTC AGG ATT GAG CTA AAG GCA TTA CTG --- --- --- --- --- --- --- --- --- --- --- --- --- ---Phe lie Tyr Cys Trp Leu Asn Giu Asn Phe Arg ile Giu Leu Lys Ala Leu Leu 1098 1107 1116 AGC ATG TGT CAA AGA CCT CCC AAG CCT CAG GAG GAC AGG CCA CCC TCC CCA GTT Ser Met Cys Gin Arg Pro Pro Lys Pro Gin Giu Asp Arg Pro Pro Ser Pro Yal 1152 1161 1170 1179 CCT TCC TTC AGG GTG GCC TGG ACA GAG AAG AAT GAT GGC CAG AGG GCT CCC CTT --- --- --- --- --- --- --- --- --- --- --- --- ---Pro Ser Phe Arg Yai Ala Trp Thr Giu Lys Asn Asp Gly Gin Arg Ala Pro Leu 1215 1224 1197 1206 1233 GCC AAT AAC CTC CTG CCC ACC TCC CAA CTC CAG TCT GGG AAG ACA GAC CTG TCA Ala Asn Asn Leu Leu Pro Thr Ser Gin Leu Gin Ser Gly Lys Thr Asp Leu Ser 1251 1260 1269 TCT GTG GAA CCC ATT GTG ACG ATG AGT TAG 3' Ser Val Glu Pro Ile Val Thr Met Ser ***



The position in the amino acid sequence

63A2. AM1 Musgir. Ami	1	10 W-VPHLLLC WKVPPVLLE	20 LLPLVRATEP LLSSVRATEO	HEGRADEOSA	40 EAALAYPNAS EAALIGPNAS	HEESWNOVIE	5 0 5 0
83A2. AMI Musgir. Ami	51 51	60 SDWONFVGRR SDWONFVGRR	70 RYGAESONPT RYGAESONPT	VKALLIVAYS VKALLIVAYS	90 Filvfslegn Friveslegn	VLVCHVIFKN VLVCHVIFKN	100 100
63A2. AMI Musgir. Ami		110 QRMHSATSLF QRMHSATSLF			140 VRFVNSTWIF VRFVNSTWVF		150 150
63A2. AMI MUSGIR. AMI	151	160 Adycslhvsa Adycslhvsa	170 LTLTAIAVDR LTLTAIAVDR	180 HQVIMHPLKP HQVIMHPLKP	190 RISITKGVIY RISITKGVIY	200 IAVIWTWATE IAVIWYWATE	200 200
63A2. AM1 MUSGIR. AMI	201	210 FSLPHAICOK FSLPHAICOK	220 Letekysedi Letekysedi	230 VASLCLPDFP VASLCLPDFP	240 EPADLFWKYL EPADLFWKYL	250 OLATFILLY OLATFILLY	250 250
63A2. AMI MUSGIR. AMI	251 251	260 LPL I I SVAY LPL FI I SVAY	270 ARVAKKLWLC ARVAKKLWLC	NMIGDYTTEO	Y = ALRRKKK	TIKMLMEVVV	300 300
63A2. AMI Musgir. Ami		310 LFALCWFPLN LFALCWFPLN					350 350
63A2. AM1 Musgir. Ami		360 Enfrielkal Enfryelkal					400 400
63A2. AMI \ MUSGIR. AMI	401 401	LLPTSQLQSG HLPSSOLQSG	420 KTOLSSVEP KTOLSSVEP	430 VTMS: VAMS:	440	450	450 450